

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
Rothstein, Steven J.  
Bowman, Cindy G.  
Dawson, John L.  
Dunder, Erik M.  
Pace, Gary M.  
Suttie, Janet L.

(ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

(iii) NUMBER OF SEQUENCES: 94

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Syngenta Biotechnology, Inc.  
(B) STREET: 3054 Cornwallis Road  
(C) CITY: Research Triangle Park  
(D) STATE: NC  
(E) COUNTRY: USA  
(F) ZIP: 27709

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/547,422  
(B) FILING DATE: 11-APR-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/459,504  
(B) FILING DATE: 02-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/951,715  
(B) FILING DATE: 25-SEP-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/772,027  
(B) FILING DATE: 04-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Meigs, J. Timothy  
(B) REGISTRATION NUMBER: 38,241  
(C) REFERENCE/DOCKET NUMBER: S-18805I

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (919)541-8587  
(B) TELEFAX: (919)541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3468 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Bacillus thuringiensis kurstaki  
(B) STRAIN: HD-1

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..3468  
(D) OTHER INFORMATION: /product= "Full-length native  
cryIA(b)"  
/note= "Appears in Figures 1 and 4 as BTHKURHD."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTTGATATAA TATGGGAAT TTTGGTCCC TCTCAATGGG ACGCATTCT TGACAAATT	240
GAACAGTTAA TTAACCAAAG AATAGAAGAA TTCGCTAGGA ACCAAGCCAT TTCTAGATTA	300
GAAGGACTAA GCAATCTTA TCAAATTAC GCAGAATCTT TTAGAGAGTG GGAAGCAGAT	360
CCTACTAAC CAGCATTAAG AGAAGAGATG CGTATTCAAT TCAATGACAT GAACAGTGCC	420
CTTACAACCG CTATTCCCTCT TTTGCAGTT CAAAATTATC AAGTTCCCTCT TTTATCAGTA	480
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AGGTGGGGAT TTGATGCCGC GACTATCAAT AGTCGTTATA ATGATTAAAC TAGGCTTATT	600
GGCAACTATA CAGATCATGC TGTACGCTGG TACAATACGG GATTAGAGCG TGTATGGGA	660
CCGGATTCTA GAGATTGGAT AAGATATAAT CAATTTAGAA GAGAATTAAC ACTAACTGTA	720
TTAGATATCG TTTCTCTATT TCCGAACAT GATAGTAGAA CGTATCCAAT TCGAACAGTT	780

TCCCAATTAA CAAGAGAAAT TTATACAAAC CCAGTATTAG AAAATTTGA TGGTAGTTT	840
CGAGGCTCGG CTCAGGGCAT AGAAGGAAGT ATTAGGAGTC CACATTTGAT GGATATACTT	900
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TACAGAAAAA GCGGAACGGT AGATTGCTG GATGAAATAC CGCCACAGAA TAACAACGTG	1260
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AGTAATAGTA GTGTAAGTAT AATAAGAGCT CCTATGTTCT CTTGGATACA TCGTAGTGCT	1380
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CGAATTGAAT TTGTTCCGGC AGAAGTAACC TTTGAGGCAG AATATGATTT AGAAAGAGCA	1860
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CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC	3060
ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTA GCAACTGTGT AGAAGAGGAA	3120
GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG	3180
GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTCTGTA	3240
CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT	3300
CCTTGTGAAT CTAACAGAGG ATATGGGAT TACACACCAC TACCAGCTGG CTATGTGACA	3360
AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA	3420
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 3468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: other nucleic acid
    - (A) DESCRIPTION: /desc = "Synthetic DNA"
  - iii) HYPOTHETICAL: NO
  - ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 1..3468
    - (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt"  
note= "Disclosed in Figure 3 as syn1T.mze"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC 240

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ACCGACTACC	ACATCGACCA	GGTGAGCAAC	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040

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 CACTTCAGCC TGGACATCGA CGTGGGCTGC ACCGACCTGA ACGAGGACCT GGGCGTGTGG 246  
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 CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCC TGCCCGCCGG CTACGTGACC 3360  
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 GGCACCTTCA TCGTGGACAG CGTGGAGCTG CTGCTGATGG AGGAGTAG 3468

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..1947  
(D) OTHER INFORMATION: /product= "Truncated synthetic maize optimized cryIA(b) gene"  
/note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC 240  
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ATCATGGCCA GCCCGCTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC 1020  
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CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC 1560  
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized"

/note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC 600

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GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
ACACCTGGGCA	GGGGCACCAAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGGGG	CGACATCCTG	1500
CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCCTGAGC	1560
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ACCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
AGCAAGCTGA	AGGCCTACAC	CCGCTACCAAG	CTGCGCGCT	ACATCGAGGA	CAGCCAGGAC	2280
CTGGAGATCT	ACCTGATCCG	CTACAACGCC	AAGCACGAGA	CCGTGAACGT	GCCCGGCACC	2340
GGCAGCCTGT	GGCCCCCTGAG	CGCCCCCAGC	CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
CACTTCAGCC	TGGACATCGA	CGTGGCTGC	ACCGACCTGA	ACGAGGACCT	GGCGTGTGG	2460

GTGATCTTCA AGATCAAGAC CCAGGACGGC CACGCCGCC TGGGCAACCT GGAGTTCTG 2520  
 GAGGAGAACG CCCTGGTGGG CGAGGCCCTG GCCCGCGTGA AGCGCGCCGA GAAGAAGTGG 2580  
 CGCGACAAGC GCGAGAAGCT GGAGTGGGAG ACCAACATCG TGTACAAGGA GGCCAAGGAG 2640  
 AGCGTGGACG CCCTGTTCGT GAACAGCCAG TACGACCGCC TGCAGGCCGA CACCAACATC 2700  
 GCCATGATCC ACGCCGCCGA CAAGCGCGTG CACAGCATTC GCGAGGCCCTA CCTGCCCGAG 2760  
 CTGAGCGTGA TCCCCGGCGT GAACGCCGCC ATCTTCGAGG AGCTGGAGGG CCGCATCTTC 2820  
 ACCGCCTTCA GCCTGTACGA CGCCCGCAAC GTGATCAAGA ACGGCGACTT CAACAACGGC 2880  
 CTGAGCTGCT GGAACGTGAA GGGCCACGTG GACGTGGAGG AGCAGAACAA CCACCGCAGC 2940  
 GTGCTGGTGG TGCCCGAGTG GGAGGCCGAG GTGAGGCCAGG AGGTGCGCGT GTGCCCGGC 3000  
 CGCGGCTACA TCCTGCGCGT GACCGCCTAC AAGGAGGGCT ACGGCGAGGG CTGCGTGACC 3060  
 ATCCACGAGA TCGAGAACAA CACCGACGAG CTCAAGTTCA GCAACTGCGT GGAGGAGGAG 3120  
 GTGTACCCCA ACAACACCGT GACCTGCAAC GACTACACCG CCACCCAGGA GGAGTACGAG 3180  
 GGCACCTACA CCAGCCGCAA CCGCGGCTAC GACGGCGCCT ACGAGAGCAA CAGCAGCGTG 3240  
 CCCGCCGACT ACGCCAGCGC CTACGAGGAG AAGGCCTACA CCGACGGCCG CCGCGACAAC 3300  
 CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCCC TGCCCGCCGG CTACGTGACC 3360  
 AAGGAGCTGG AGTACTTCCC CGAGACCGAC AAGGTGTGGA TCGAGATCGG CGAGACCGAG 3420  
 GGCACCTTCA TCGTGGACAG CGTGGAGCTG CTGCTGATGG AGGAGTAG 3468

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1845
- (D) OTHER INFORMATION: /note= "This is the synthetic Bt gene according to Perlak et al. as shown in Figures 4 and 5 as PMONBT."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACAACA ACCCAAACAT CAACGAATGC ATTCCATACA ACTGCTTGAG TAACCCAGAA

60

GTTGAAGTAC TTGGTGGAGA ACGCATTGAA ACCGGTTACA CTCCCATCGA CATCTCCTG	120
TCCTTGACAC AGTTTCTGCT CAGCGAGTTC GTGCCAGGTG CTGGGTCGT TCTCGGACTA	180
GTTGACATCA TCTGGGTAT CTTTGGTCCA TCTCAATGGG ATGCATTCT GGTGCAAATT	240
GAGCAGTTGA TCAACCAGAG GATCGAAGAG TTCGCCAGGA ACCAGGCCAT CTCTAGGTTG	300
GAAGGATTGA GCAATCTCTA CCAAATCTAT GCAGAGAGCT TCAGAGAGTG GGAAGCCGAT	360
CCTACTAACCC CAGCTCTCCG CGAGGAAATG CGTATTCAAT TCAACGACAT GAACAGCGCC	420
TTGACCACAG CTATCCCATT GTTCGCAGTC CAGAACTACC AAGTTCCCTCT CTTGTCCGTG	480
TACGTTCAAG CAGCTAATCT TCACCTCAGC GTGCTTCAGAG ACGTTAGCGT GTTGGGCAA	540
AGGTGGGGAT TCGATGCTGC AACCATCAAT AGCCGTTACA ACGACCTTAC TAGGCTGATT	600
GGAAACTACA CCGACCACGC TGTCGTTGG TACAACACTG GCTTGGAGCG TGTCTGGGT	660
CCTGATTCTA GAGATTGGAT TAGATACAAC CAGTTCAGGA GAGAATTGAC CCTCACAGTT	720
TTGGACATTG TGTCTCTCTT CCCGAACTAT GACTCCAGAA CCTACCCTAT CCGTACAGTG	780
TCCCAACTTA CCAGAGAAAT CTATACTAAC CCAGTTCTG AGAACTTCGA CGGTAGCTTC	840
CGTGGTTCTG CCCAAGGTAT CGAAGGCTCC ATCAGGAGCC CACACTTGAT GGACATCTG	900
AACAGCATAA CTATCTACAG CGATGCTCAC AGAGGGAGGT ATTACTGGTC TGGACACCAG	960
ATCATGGCCT CTCCAGTTGG ATTCAAGCGGG CCCGAGTTA CCTTTCCCTCT CTATGGAAC	1020
ATGGGAAACG CCGCTCCACA ACAACGTATC GTTGCTAAC TAGGTCAGGG TGTCTACAGA	1080
ACCTTGTCTT CCACCTTGTA CAGAAGACCC TTCAATATCG GTATCAACAA CCAGCAACTT	1140
TCCGTTCTTG ACGGAACAGA GTTCGCCTAT GGAACCTCTT CTAACTTGCC ATCCGCTGTT	1200
TACAGAAAGA GCGGAACCGT TGATTCCCTG GACGAAATCC CACCACAGAA CAACAATGTG	1260
CCACCCAGGC AAGGATTCTC CCACAGGTTG AGCCACGTGT CCATGTTCCG TTCCGGATTC	1320
AGCAACAGTT CCGTGAGCAT CATCAGAGCT CCTATGTTCT CATGGATTCA TCGTAGTGCT	1380
GAGTTCAACA ATATCATTCC TTCCCTCTCAA ATCACCCAAA TCCCATTGAC CAAGTCTACT	1440
AACCTGGAT CTGGAACCTTC TGTCGTGAAA GGACCAGGCT TCACAGGAGG TGATATTCTT	1500
AGAAGAACTT CTCCTGGCCA GATTAGCACC CTCAGAGTTA ACATCACTGC ACCACTTCT	1560
CAAAGATATC GTGTCAGGAT TCGTTACGCA TCTACCACTA ACTTGCAATT CCACACCTCC	1620
ATCGACGGAA GGCCTATCAA TCAGGGTAAC TTCTCCGCAA CCATGTCAAG CGGCAGCAAC	1680
TTGCAATCCG GCAGCTTCAG AACCGTCGGT TTCACTACTC CTTTCAACTT CTCTAACGGA	1740
TCAAGCGTTT TCACCCCTAG CGCTCATGTG TTCAATTCTG GCAATGAAGT GTACATTGAC	1800
CGTATTGAGT TTGTGCCTGC CGAAGTTACC TTCAAGGCTG AGTAC	1845

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3624 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..3621  
(D) OTHER INFORMATION: /product= "Full-length, maize  
optimized cryIB"  
/note= "Disclosed in Figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAC CTG CTG CCC GAC GCC CGC ATC GAG GAC AGC CTG TGC ATC GCC	48
Met Asp Leu Leu Pro Asp Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala	
1 5 10 15	
GAG GGC AAC AAC ATC GAC CCC TTC GTG AGC GCC AGC ACC GTG CAG ACC	96
Glu Gly Asn Asn Ile Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr	
20 25 30	
GGC ATC AAC ATC GCC GGC CGC ATC CTG GGC GTG CTG GGC GTG CCC TTC	144
Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe	
35 40 45	
GCC GGC CAG CTG GCC AGC TTC TAC AGC TTC CTG GTG GGC GAG CTG TGG	192
Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp	
50 55 60	
CCC CGC GGC CGC GAC CAG TGG GAG ATC TTC CTG GAG CAC GTG GAG CAG	240
Pro Arg Gly Arg Asp Gln Trp Glu Ile Phe Leu Glu His Val Glu Gln	
65 70 75 80	
CTG ATC AAC CAG CAG ATC ACC GAG AAC GCC CGC AAC ACC GCC CTG GCC	288
Leu Ile Asn Gln Ile Thr Glu Asn Ala Arg Asn Thr Ala Leu Ala	
85 90 95	
CGC CTG CAG GGC CTG GGC GAC AGC TTC CGC GCC TAC CAG CAG AGC CTG	336
Arg Leu Gln Gly Leu Gly Asp Ser Phe Arg Ala Tyr Gln Gln Ser Leu	
100 105 110	
GAG GAC TGG CTG GAG AAC CGC GAC GAC GCC CGC ACC CGC AGC GTG CTG	384
Glu Asp Trp Leu Glu Asn Arg Asp Asp Ala Arg Thr Arg Ser Val Leu	
115 120 125	
TAC ACC CAG TAC ATC GCC CTG GAG CTG GAC TTC CTG AAC GCC ATG CCC	432
Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro	
130 135 140	
CTG TTC GCC ATC CGC AAC CAG GAG GTG CCC CTG CTG ATG GTG TAC GCC	480
Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala	

145	150	155	160	
CAG GCC GCC AAC CTG CAC CTG CTG CTG CGC GAC GCC AGC CTG TTC Gln Ala Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Leu Phe 165 170 175				528
Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu 180 185 190				576
CGC CAG GTG GAG CGC ACC CGC GAC TAC AGC GAC TAC TGC GTG GAG TGG Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp 195 200 205				624
TAC AAC ACC GGC CTG AAC AGC CTG CGC GGC ACC AAC GCC GCC AGC TGG Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp 210 215 220				672
GTG CGC TAC AAC CAG TTC CGC CGC GAC CTG ACC CTG GGC GTG CTG GAC Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp 225 230 235 240				720
CTG GTG GCC-CTG TTC CCC AGC TAC GAC ACC CGC ACC TAC CCC ATC AAC Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn 245 250 255				768
ACC AGC GCC CAG CTG ACC CGC GAG GTG TAC ACC GAC GCC ATC GGC GCC Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala 260 265 270				816
ACC GGC GTG AAC ATG GCC AGC ATG AAC TGG TAC AAC AAC AAC GCC CCC Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro 275 280 285				864
AGC TTC AGC GCC ATC GAG GCC GCC ATC CGC AGC CCC CAC CTG CTG Ser Phe Ser Ala Ile Glu Ala Ala Ile Arg Ser Pro His Leu Leu 290 295 300				912
GAC TTC CTG GAG CAG CTG ACC ATC TTC AGC GCC AGC AGC CGC TGG AGC Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser 305 310 315 320				960
AAC ACC CGC CAC ATG ACC TAC TGG CGC GGC CAC ACC ATC CAG AGC CGC Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg 325 330 335				1008
CCC ATC GGC GGC CTG AAC ACC AGC ACC CAC GGC GCC ACC AAC ACC Pro Ile Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr 340 345 350				1056
AGC ATC AAC CCC GTG ACC CTG CGC TTC GCC AGC CGC GAC GTG TAC CGC Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg 355 360 365				1104
ACC GAG AGC TAC GCC GGC GTG CTG CTG TGG GGC ATC TAC CTG GAG CCC Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro 370 375 380				1152
ATC CAC GGC GTG CCC ACC GTG CGC TTC AAC TTC ACC AAC CCC CAG AAC Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn 385 390 395 400				1200

ATC AGC GAC CGC GGC ACC GCC AAC TAC AGC CAG CCC TAC GAG AGC CCC Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro 405 410 415	1245
GGC CTG CAG CTG AAG GAC AGC GAG ACC GAG CTG CCC CCC GAG ACC ACC Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr 420 425 430	1295
GAG CGC CCC AAC TAC GAG AGC TAC AGC CAC CGC CTG AGC CAC ATC GGC Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly 435 440 445	1345
ATC ATC CTG CAG AGC CGC GTG AAC GTG CCC GTG TAC AGC TGG ACC CAC Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His 450 455 460	1392
CGC AGC GCC GAC CGC ACC AAC ACC ATC GGC CCC AAC CGC ATC ACC CAG Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln 465 470 475 480	1440
ATC CCC ATG GTG AAG GCC AGC GAG CTG CCC CAG GGC ACC ACC GTG GTG Ile Pro Met Val Lys Ala Ser Glu Leu Pro Gln Gly Thr Thr Val Val 485 490 495	1485
CGC GGC CCC GGC TTC ACC GGC GGC GAC ATC CTG CGC CGC ACC AAC ACC Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr 500 505 510	1536
GGC GGC TTC GGC CCC ATC CGC GTG ACC GTG AAC GGC CCC CTG ACC CAG Gly Gly Phe Gly Pro Ile Arg Val Thr Val Asn Gly Pro Leu Thr Gln 515 520 525	1585
CGC TAC CGC ATC GGC TTC CGC TAC GCC AGC ACC GTG GAC TTC GAC TTC Arg Tyr Arg Ile Gly Phe Arg Tyr Ala Ser Thr Val Asp Phe Asp Phe 530 535 540	1632
TTC GTG AGC CGC GGC GGC ACC ACC GTG AAC AAC TTC CGC TTC CTG CGC Phe Val Ser Arg Gly Gly Thr Thr Val Asn Asn Phe Arg Phe Leu Arg 545 550 555 560	1680
ACC ATG AAC AGC GGC GAC GAG CTG AAG TAC GGC AAC TTC GTG CGC CGC Thr Met Asn Ser Gly Asp Glu Leu Lys Tyr Gly Asn Phe Val Arg Arg 565 570 575	1728
GCC TTC ACC ACC CCC TTC ACC ACC CAG ATC CAG GAC ATC ATC CGC Ala Phe Thr Thr Pro Phe Thr Phe Thr Gln Ile Gln Asp Ile Ile Arg 580 585 590	1776
ACC AGC ATC CAG GGC CTG AGC GGC AAC GGC GAG GTG TAC ATC GAC AAG Thr Ser Ile Gln Gly Leu Ser Gly Asn Gly Glu Val Tyr Ile Asp Lys 595 600 605	1824
ATC GAG ATC ATC CCC GTG ACC GCC ACC TTC GAG GCC GAG TAC GAC CTG Ile Glu Ile Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu 610 615 620	1872
GAG CGC GCC CAG GAG GCC GTG AAC GCC CTG TTC ACC AAC ACC AAC CCC Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe Thr Asn Thr Asn Pro 625 630 635 640	1920

CGC CGC CTG AAG ACC GAC GTG ACC GAC TAC CAC ATC GAC CAG GTG AGC		1968
Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser		
645	650	655
AAC CTG GTG GCC TGC CTG AGC GAC GAG TTC TGC CTG GAC GAG AAG CGC		2015
Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg		
660	665	670
GAG CTG CTG GAG AAG GTG AAG TAC GCC AAG CGC CTG AGC GAC GAG CGC		2064
Glu Leu Leu Glu Lys Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg		
675	680	685
AAC CTG CTG CAG GAC CCC AAC TTC ACC AGC ATC AAC AAG CAG CCC GAC		2112
Asn Leu Leu Gln Asp Pro Asn Phe Thr Ser Ile Asn Lys Gln Pro Asp		
690	695	700
TTC ATC AGC ACC AAC GAG CAG AGC AAC TTC ACC AGC ATC CAC GAG CAG		2160
Phe Ile Ser Thr Asn Glu Gln Ser Asn Phe Thr Ser Ile His Glu Gln		
705	710	715
720		
AGC GAG CAC GGC TGG TGG GGC AGC GAG AAC ATC ACC ATC CAG GAG GGC		2203
Ser Glu His Gly Trp Trp Gly Ser Glu Asn Ile Thr Ile Gln Glu Gly		
725	730	735
AAC GAC GTG TTC AAG GAG AAC TAC GTG ACC CTG CCC GGC ACC TTC AAC		2256
Asn Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn		
740	745	750
GAG TGC TAC CCC ACC TAC CTG TAC CAG AAG ATC GGC GAG AGC GAG CTG		2304
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu		
755	760	765
AAG GCC TAC ACC CGC TAC CAG CTG CGC GGC TAC ATC GAG GAC AGC CAG		2352
Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln		
770	775	780
GAC CTG GAG ATC TAC CTG ATC CGC TAC AAC GCC AAG CAC GAG ACC CTG		2400
Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu		
785	790	795
800		
GAC GTG CCC GGC ACC GAG AGC CTG TGG CCC CTG AGC GTG GAG AGC CCC		2448
Asp Val Pro Gly Thr Glu Ser Leu Trp Pro Leu Ser Val Glu Ser Pro		
805	810	815
ATC GGC CGC TGC GGC GAG CCC AAC CGC TGC GCC CCC CAC TTC GAG TGG		2496
Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp		
820	825	830
AAC CCC GAC CTG GAC TGC AGC TGC CGC GAC GGC GAG AAG TGC GCC CAC		2544
Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His		
835	840	845
CAC AGC CAC CAC TTC AGC CTG GAC ATC GAC GTG GGC TGC ACC GAC CTG		2592
His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu		
850	855	860
CAC GAG AAC CTG GGC GTG TGG GTG GTG TTC AAG ATC AAG ACC CAG GAG		2640
His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu		
865	870	875
880		
GGC CAC GCC CGC CTG GGC AAC CTG GAG TTC ATC GAG GAG AAG CCC CTG		2688

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu		
885 890 895		
CTG GGC GAG GCC CTG AGC CGC GTG AAG CGC GCC GAG AAG AAG TGG CGC	2736	
Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg		
900 905 910		
GAC AAG CGC GAG AAG CTG CAG CTG GAG ACC AAG CGC GTG TAC ACC GAG	2784	
Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu		
915 920 925		
GCC AAG GAG GCC GTG GAC GCC CTG TTC GTG GAC AGC CAG TAC GAC CGC	2832	
Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg		
930 935 940		
CTG CAG GCC GAC ACC AAC ATC GGC ATG ATC CAC GCC GCC GAC AAG CTG	2880	
Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu		
945 950 955 960		
GTG CAC CGC ATC CGC GAG GCC TAC CTG AGC GAG CTG CCC GTG ATC CCC	2928	
Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro		
965 970 975		
GGC GTG AAC GCC GAG ATC TTC GAG GAG CTG GAG GGC CAC ATC ATC ACC	2976	
Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr		
980 985 990		
GCC ATC AGC CTG TAC GAC GCC CGC AAC GTG GTG AAG AAC GGC GAC TTC	3024	
Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe		
995 1000 1005		
AAC AAC GGC CTG ACC TGC TGG AAC GTG AAG GGC CAC GTG GAC GTG CAG	3072	
Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln		
1010 1015 1020		
CAG AGC CAC CAC CGC AGC GAC CTG GTG ATC CCC GAG TGG GAG GCC GAG	3120	
Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu		
1025 1030 1035 1040		
GTG AGC CAG GCC GTG CGC GTG TGC CCC GGC TGC GGC TAC ATC CTG CGC	3168	
Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg		
1045 1050 1055		
GTG ACC GCC TAC AAG GAG GGC TAC GGC GAG GGC TGC GTG ACC ATC CAC	3216	
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His		
1060 1065 1070		
GAG ATC GAG AAC AAC ACC GAC GAG CTG AAG TTC AAG AAC CGC GAG GAG	3264	
Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu		
1075 1080 1085		
GAG GAG GTG TAC CCC ACC GAC ACC GGC ACC TGC AAC GAC TAC ACC GCC	3312	
Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala		
1090 1095 1100		
CAC CAG GGC ACC GCC GGC TGC GCC GAC GCC TGC AAC AGC CGC AAC GCC	3360	
His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala		
1105 1110 1115 1120		
GGC TAC GAG GAC GCC TAC GAG GTG GAC ACC ACC GCC AGC GTG AAC TAC	3408	
Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr		

1125	1130	1135	
AAG CCC ACC TAC GAG GAG GAG ACC	TAC ACC GAC GTG CGC CGC GAC AAC		3456
Lys Pro Thr Tyr Glu Glu Glu Thr	Tyr Thr Asp Val Arg Arg Asp Asn		
1140	1145	1150	
CAC TGC GAG TAC GAC CGC GGC TAC GTG AAC TAC CCC CCC GTG CCC GCC			3504
His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala			
1155	1160	1165	
GCG TAC GTG ACC AAG GAG CTG GAG TAC TTC CCC GAG ACC GAC ACC GTG			3552
Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val			
1170	1175	1180	
TGG ATC GAG ATC GGC GAG ACC GAG GGC AAG TTC ATC GTG GAC AGC GTG			3600
Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val			
1185	1190	1195	1200
GAG CTG CTG CTG ATG GAG GAG TAG			3624
Glu Leu Leu Leu Met Glu Glu			
1205			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Leu Leu Pro Asp Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala			
1	5	10	15
Glu Gly Asn Asn Ile Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr			
20		25	30
Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe			
35	40	45	
Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp			
50	55	60	
Pro Arg Gly Arg Asp Gln Trp Glu Ile Phe Leu Glu His Val Glu Gln			
65	70	75	80
Leu Ile Asn Gln Gln Ile Thr Glu Asn Ala Arg Asn Thr Ala Leu Ala			
85		90	95
Arg Leu Gln Gly Leu Gly Asp Ser Phe Arg Ala Tyr Gln Gln Ser Leu			
100	105	110	
Glu Asp Trp Leu Glu Asn Arg Asp Asp Ala Arg Thr Arg Ser Val Leu			
115	120	125	
Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro			
130	135	140	

Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala  
145 150 155 160

Gln Ala Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Leu Phe  
165 170 175

Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu  
180 185 190

Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp  
195 200 205

Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp  
210 215 220

Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp  
225 230 235 240

Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn  
245 250 255

Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala  
260 265 270

Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro  
275 280 285

Ser Phe Ser Ala Ile Glu Ala Ala Ile Arg Ser Pro His Leu Leu  
290 295 300

Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser  
305 310 315 320

Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg  
325 330 335

Pro Ile Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr  
340 345 350

Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg  
355 360 365

Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro  
370 375 380

Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn  
385 390 395 400

Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro  
405 410 415

Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr  
420 425 430

Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly  
435 440 445

Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His  
450 455 460

Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

465                    470                    475                    480  
Ile Pro Met Val Lys Ala Ser Glu Leu Pro Gln Gly Thr Thr Val Val  
485                    490                    495  
Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr  
500                    505                    510  
Gly Gly Phe Gly Pro Ile Arg Val Thr Val Asn Gly Pro Leu Thr Gln  
515                    520                    525  
Arg Tyr Arg Ile Gly Phe Arg Tyr Ala Ser Thr Val Asp Phe Asp Phe  
530                    535                    540  
Phe Val Ser Arg Gly Gly Thr Thr Val Asn Asn Phe Arg Phe Leu Arg  
545                    550                    555                    560  
Thr Met Asn Ser Gly Asp Glu Leu Lys Tyr Gly Asn Phe Val Arg Arg  
565                    570                    575  
Ala Phe Thr Thr Pro Phe Thr Phe Thr Gln Ile Gln Asp Ile Ile Arg  
580                    585                    590  
Thr Ser Ile Gln Gly Leu Ser Gly Asn Gly Glu Val Tyr Ile Asp Lys  
595                    600                    605  
Ile Glu Ile Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr Asp Leu  
610                    615                    620  
Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe Thr Asn Thr Asn Pro  
625                    630                    635                    640  
Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser  
645                    650                    655  
Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg  
660                    665                    670  
Glu Leu Leu Glu Lys Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg  
675                    680                    685  
Asn Leu Leu Gln Asp Pro Asn Phe Thr Ser Ile Asn Lys Gln Pro Asp  
690                    695                    700  
Phe Ile Ser Thr Asn Glu Gln Ser Asn Phe Thr Ser Ile His Glu Gln  
705                    710                    715                    720  
Ser Glu His Gly Trp Trp Gly Ser Glu Asn Ile Thr Ile Gln Glu Gly  
725                    730                    735  
Asn Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn  
740                    745                    750  
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu  
755                    760                    765  
Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln  
770                    775                    780  
Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu  
785                    790                    795                    800

Asp Val Pro Gly Thr Glu Ser Leu Trp Pro Leu Ser Val Glu Ser Pro  
 805 810 815  
 Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp  
 820 825 830  
 Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His  
 835 840 845  
 His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu  
 850 855 860  
 His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu  
 865 870 875 880  
 Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu  
 885 890 895  
 Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg  
 900 905 910  
 Asp Lys Arg-Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu  
 915 920 925  
 Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg  
 930 935 940  
 Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu  
 945 950 955 960  
 Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro  
 965 970 975  
 Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr  
 980 985 990  
 Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe  
 995 1000 1005  
 Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln  
 1010 1015 1020  
 Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu  
 1025 1030 1035 1040  
 Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg  
 1045 1050 1055  
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His  
 1060 1065 1070  
 Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu  
 1075 1080 1085  
 Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala  
 1090 1095 1100  
 His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala  
 1105 1110 1115 1120

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr  
1125 1130 1135

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn  
1140 1145 1150

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala  
1155 1160 1165

Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val  
1170 1175 1180

Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val  
1185 1190 1195 1200

Glu Leu Leu Leu Met Glu Glu  
1205

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3465
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
partially maize optimized cryIA(b)"  
/note= "Disclosed in Figure 7 as contained in pCIB4434."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG  
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 48  
1210 1215 1220

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC  
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 96  
1225 1230 1235

TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC  
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 144  
1240 1245 1250 1255

GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC  
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 192  
1260 1265 1270

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC  
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 240  
1275 1280 1285

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1290 1295 1300	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1305 1310 1315	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1320 1325 1330 1335	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1340 1345 1350	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1355 1360 1365	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1370 1375 1380	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1385 1390 1395	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1400 1405 1410 1415	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1420 1425 1430	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1435 1440 1445	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1450 1455 1460	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1465 1470 1475	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1480 1485 1490 1495	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1500 1505 1510	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1515 1520 1525	960

FOOTER

ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1530 1535 1540	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1545 1550 1555	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1560 1565 1570 1575	1104
CGA CCT TTC AAC ATC GGC ATC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1580 1585 1590	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1595 1600 1605	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1610 1615 1620	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1625 1630 1635	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Val Ser Ile Ile 1640 1645 1650 1655	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1660 1665 1670	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1675 1680 1685	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1690 1695 1700	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1705 1710 1715	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1720 1725 1730 1735	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1740 1745 1750	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1755 1760 1765	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC	1728

Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
1770					1775						1780					
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
1785					1790					1795						
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
1800			1805				1810						1815			
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
1820					1825			1830								
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
1835					1840			1845								
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
1850					1855			1860								
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
1865					1870			1875								
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
1880					1885			1890								
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
1900					1905			1910								
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
1915					1920			1925								
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
1930					1935			1940								
AAA	ATA	GAT	GAG	TCG	AAA	TTA	AAA	GCC	TAT	ACC	CGT	TAC	CAA	TTA	AGA	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
1945					1950			1955								
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
1960					1965			1970								
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
1980					1985			1990								
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGA	AAA	TGT	GCC	CAT	CAT	TCC	CAT	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Ala	His	His	Ser	His	
1995					2000			2005								
CAT	TTC	TCC	TTG	GAC	ATT	GAT	GTT	GGA	TGT	ACA	GAC	TTA	AAT	GAG	GAC	2448
His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	

2001-2002-2003-2004-2005

2010	2015	2020	
TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala 2025	2030	2035	2496
AGA CTA GGA AAT CTA GAA TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA Arg Leu Gly Asn Leu Glu Phe Leu Glu Lys Pro Leu Val Gly Glu 2040	2045	2050	2544
GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg 2060	2065	2070	2592
GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu 2075	2080	2085	2640
TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala 2090	2095	2100	2688
GAT ACC AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser 2105	2110	2115	2736
ATT CGA GAA GCT TAT CTG CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn 2120	2125	2130	2784
GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser 2140	2145	2150	2832
CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly 2155	2160	2165	2880
TTA TCC TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn 2170	2175	2180	2928
AAC CAC CGT TCG GTC CTT GTT CCG GAA TGG GAA GCA GAA GTG TCA Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser 2185	2190	2195	2976
CAA GAA GTT CGT GTC TGT CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr 2200	2205	2210	3024
GCG TAC AAG GAG GGA TAT GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile 2220	2225	2230	3072
GAG AAC AAT ACA GAC GAA CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu 2235	2240	2245	3120
GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln 2250	2255	2260	3168

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GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly 2265 2270 2275	3216
GCC TAT GAA AGC AAT TCT TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT Ala Tyr Glu Ser Asn Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr 2280 2285 2290 2295	3264
GAA GAA AAA GCA TAT ACA GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser 2300 2305 2310	3312
AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr 2315 2320 2325	3360
AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile 2330 2335 2340	3408
GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu 2345 2350 2355	3456
ATG GAG GAA TAA Met Glu Glu 2360	3468

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr

755

760

765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
 770 775 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Ala His His Ser His  
 785 790 795 800

His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp  
 805 810 815

Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala  
 820 825 830

Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu  
 835 840 845

Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg  
 850 855 860

Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu  
 865 870 875 880

Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala  
 885 890 895

Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser  
 900 905 910

Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn  
 915 920 925

Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser  
 930 935 940

Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly  
 945 950 955 960

Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn  
 965 970 975

Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser  
 980 985 990

Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr  
 995 1000 1005

Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile  
 1010 1015 1020

Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu  
 1025 1030 1035 1040

Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln  
 1045 1050 1055

Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly  
 1060 1065 1070

Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr  
 1075 1080 1085

Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asn Pro Cys Glu Ser  
 1090 1095 1100  
 Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr  
 1105 1110 1115 1120  
 Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile  
 1125 1130 1135  
 Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu  
 1140 1145 1150  
 Met Glu Glu  
 1155

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
maize optimized heat stable cryIA(b)"  
/note= "Disclosed in Figure 9 as contained in pCIB5511."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1160 1165 1170	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1175 1180 1185	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1190 1195 1200	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1205 1210 1215	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1220 1225 1230 1235	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
 1240 1245 1250

ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG 336  
 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
 1255 1260 1265

AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG 384  
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
 1270 1275 1280

GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC 432  
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
 1285 1290 1295

ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG 480  
 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
 1300 1305 1310 1315

TAC GTG CAG GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC 528  
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
 1320 1325 1330

GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC ACC ATC AAC AGC CGC 576  
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
 1335 1340 1345

TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG 624  
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
 1350 1355 1360

CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC 672  
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
 1365 1370 1375

GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG 720  
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
 1380 1385 1390 1395

CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC 768  
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
 1400 1405 1410

ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG 816  
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
 1415 1420 1425

CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG 864  
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
 1430 1435 1440

GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC 912  
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
 1445 1450 1455

ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG 960  
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
 1460 1465 1470 1475

ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC 1008  
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro

1480	1485	1490	
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1495	1500	1505	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1510	1515	1520	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1525	1530	1535	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1540	1545	1550	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1560	1565	1570	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1575	1580	1585	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1590	1595	1600	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1605	1610	1615	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1620	1625	1630	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1640	1645	1650	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1655	1660	1665	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1670	1675	1680	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1685	1690	1695	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1700	1705	1710	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1720	1725	1730	1728

TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 1735 1740 1745	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1750 1755 1760	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1765 1770 1775	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1780 1785 1790 1795	1920
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1800 1805 1810	1968
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1815 1820 1825	2016
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1830 1835 1840	2064
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 1845 1850 1855	2112
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT Asp Ile Thr Ile Gln Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1860 1865 1870 1875	2160
ACG CTA TTG GGT ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1880 1885 1890	2208
AAG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1895 1900 1905	2256
GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 1910 1915 1920	2304
AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 1925 1930 1935	2352
CCC CTG AGC GCC CCC AGC CCC ATC GGC AAG TGC GGG GAG CCG AAT CGA Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 1940 1945 1950 1955	2400
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1960 1965 1970	2448

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GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 1975 1980 1985	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 1990 1995 2000	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2005 2010 2015	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2020 2025 2030 2035	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2040 2045 2050	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe - 2055 2060 2065	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2070 2075 2080	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2085 2090 2095	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2100 2105 2110 2115	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2120 2125 2130	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2135 2140 2145	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2150 2155 2160	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2165 2170 2175	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2180 2185 2190 2195	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2200 2205 2210	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG	3216

Leu Lys Phe Ser Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr			
2215	2220	2225	
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG		3264	
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Tyr Glu Gly Thr			
2230	2235	2240	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT		3312	
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser			
2245	2250	2255	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA		3360	
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr			
2260	2265	2270	2275
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT		3408	
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp			
2280	2285	2290	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC		3456	
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe			
2295	2300	2305	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA		3504	
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr			
2310	2315	2320	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA		3546	
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu			
2325	2330	2335	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu			
1	5	10	15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly			
20	25	30	
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser			
35	40	45	
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile			
50	55	60	
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile			
65	70	75	80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala			
85	90	95	

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
 100 105 110  
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
 115 120 125  
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
 130 135 140  
 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
 145 150 155 160  
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
 165 170 175  
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
 180 185 190  
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
 195 200 205  
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
 210 215 220  
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
 225 230 235 240  
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
 245 250 255  
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
 260 265 270  
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
 275 280 285  
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
 290 295 300  
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
 305 310 315 320  
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
 325 330 335  
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
 340 345 350  
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
 355 360 365  
 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
 370 375 380  
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 385 390 395 400  
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 405 410 415  
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His

420

425

430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
 500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
 515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
 545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
 565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
 580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
 595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
 610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
 625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
 645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
 660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
 690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
 705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
 725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
 740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
770 775 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg  
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg  
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile  
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys  
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu  
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu  
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val  
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr  
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
 1075 1080 1085  
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
 1090 1095 1100  
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
 1105 1110 1115 1120  
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
 1125 1130 1135  
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
 1140 1145 1150  
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
 1155 1160 1165  
 Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
maize optimized heat stable cryIA(b)"  
/note= "Disclosed in Figure 11 as contained in pCIB5512"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185 1190 1195	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200 1205 1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215 1220 1225	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1230 1235 1240 1245	

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	960

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
 1490 1495 1500

ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC  
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
 1505 1510 1515

1008

CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA  
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
 1520 1525 1530

1056

CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT  
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
 1535 1540 1545

1104

CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC  
 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Leu Ser Val Leu Asp  
 1550 1555 1560 1565

1152

GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG  
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 1570 1575 1580

1200

TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG  
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 1585 1590 1595

1248

AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC  
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
 1600 1605 1610

1296

GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC  
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 1615 1620 1625

1344

CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC  
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 1630 1635 1640 1645

1392

ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC  
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 1650 1655 1660

1440

AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC  
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 1665 1670 1675

1488

GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC  
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
 1680 1685 1690

1536

GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC  
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
 1695 1700 1705

1584

TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC  
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 1710 1715 1720 1725

1632

CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC  
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn

1680

1730	1735	1740	
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1745	1750	1755	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 1760	1765	1770	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1775	1780	1785	1824
GTC ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1790	1795	1800	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1810	1815	1820	1920
ACC GAC TAC CAC ATC GAT CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1825	1830	1835	1968
GAC GAG TTC TGC CTG GAC GAG AAG AAG GAG CTG AGC GAG AAG GTG AAG Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1840	1845	1850	2016
CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1855	1860	1865	2064
TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 1870	1875	1880	2112
GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG Asp Ile Thr Ile Gln Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1890	1895	1900	2160
ACC CTG CTG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1905	1910	1915	2208
AAG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1920	1925	1930	2256
GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 1935	1940	1945	2304
AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 1950	1955	1960	2352
CCC CTG AGC GCC CCC AGC CCC ATC GGC AAG TGC GGG GAG CCG AAT CGA Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 1970	1975	1980	2400

TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005 2010	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	2544
TTC AAG ATC AAG ACC CAG GAC GCC CAC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120

GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1181 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein
  - xii) SEQUENCE DESCRIPTION: SEO ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu  
1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly  
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser  
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile  
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

65                    70                    75                    80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
85                    90                    95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
100                    105                    110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115                    120                    125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130                    135                    140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145                    150                    155                    160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165                    170                    175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180                    185                    190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195                    200                    205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210                    215                    220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225                    230                    235                    240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245                    250                    255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260                    265                    270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275                    280                    285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290                    295                    300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305                    310                    315                    320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325                    330                    335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
340                    345                    350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
355                    360                    365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
370                    375                    380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
385                    390                    395                    400

TOPCAT

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
 725 730 735  
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
 740 745 750  
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
 755 760 765  
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
 770 775 780  
 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg  
 785 790 795 800  
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg  
 805 810 815  
 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile  
 820 825 830  
 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
 835 840 845  
 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
 850 855 860  
 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys  
 865 870 875 880  
 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu  
 885 890 895  
 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
 900 905 910  
 Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
 915 920 925  
 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu  
 930 935 940  
 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
 945 950 955 960  
 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
 965 970 975  
 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val  
 980 985 990  
 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
 995 1000 1005  
 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
 1010 1015 1020  
 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
 1025 1030 1035 1040  
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu

1045	1050	1055
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr		
1060	1065	1070
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr		
1075	1080	1085
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser		
1090	1095	1100
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr		
1105	1110	1115
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp		
1125	1130	1135
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe		
1140	1145	1150
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr		
1155	1160	1165
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu		
1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
maize optimized heat stable cryIA(b)"  
/note= "Disclosed in Figure 13 as contained in pCIB5513."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48	
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu		
1185	1190	1195
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96	
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly		
1200	1205	1210
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144	
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser		
1215	1220	1225

99533442001

GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864

GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC ACC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1525 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1555 1560 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1575 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695 1700 1705	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC	1632

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 1710 1715 1720 1725  
 CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC 1680  
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
 1730 1735 1740  
 CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC 1728  
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
 1745 1750 1755  
 TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC 1776  
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
 1760 1765 1770  
 AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG 1824  
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
 1775 1780 1785  
 GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG 1872  
 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
 1790 1795 1800 1805  
 AAC GAG CTG TTC ACC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG 1920  
 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
 1810 1815 1820  
 ACC GAC TAC CAC ATC GAC CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC 1968  
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
 1825 1830 1835  
 GAC GAG TTC TGC CTG GAC GAG AAG GAG CTG AGC GAG AAG GTG AAG 2016  
 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
 1840 1845 1850  
 CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC 2064  
 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 1855 1860 1865  
 TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC 2112  
 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
 1870 1875 1880 1885  
 GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG 2160  
 Asp Ile Thr Ile Gln Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
 1890 1895 1900  
 ACC CTG CAG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG 2208  
 Thr Leu Gln Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
 1905 1910 1915  
 CCG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC 2256  
 Pro Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
 1920 1925 1930  
 GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC 2304  
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
 1935 1940 1945  
 AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG 2352  
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp

DRAFT 2001

1950	1955	1960	1965	
CCC CTG AGC GCC CCC AGC CCC ATC GGC AAG TGC GGG GAG CCG AAT CGA Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 1970 1975 1980				2400
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995				2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His Phe Ser Leu Asp Ile 2000 2005 2010				2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025				2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAG Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045				2592
TTC CTG GAG GAG AAG CCC CTG GTG GGC GAG GCC CTG GCC CGC GTG AAG Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060				2640
CGC GCC GAG AAG AAG TGG CGC GAC AAG CGC GAG AAG CTG GAG TGG GAG Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075				2688
ACC AAC ATC GTG TAC AAG GAG GCC AAG GAG AGC GTG GAC GCC CTG TTC Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090				2736
GTG AAC AGC CAG TAC GAC CGC CTG CAG GCC GAC ACC AAC ATC GCC ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105				2784
ATC CAC GCC GCC GAC AAG CGC GTG CAC AGC ATT CGC GAG GCC TAC CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125				2832
CCC GAG CTG AGC GTG ATC CCC GGC GTG AAC GCC GCC ATC TTC GAG GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140				2880
CTC GAG GGC CGC ATC TTC ACC GCC TTC AGC CTG TAC GAC GCC CGC AAC Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155				2928
GTG ATC AAG AAC GGC GAC TTC AAC AAC GGC CTG AGC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170				2976
AAG GGC CAC GTG GAC GTG GAG GAG CAG AAC AAC CAC CGC AGC GTG CTG Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185				3024
GTG GTG CCC GAG TGG GAG GCC GAG GTG AGC CAG GAG GTG CGC GTG TGC Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205				3072

CCC GGC CGC GGC TAC ATC CTG CGC GTG ACC GCC TAC AAG GAG GGC TAC Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120
GGC GAG GGC TGC GTG ACC ATC CAC GAG ATC GAG AAC AAC ACC GAC GAG Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTC AAG TTC AGC AAC TGC GTG GAG GAG GTT TAC CCC AAC AAC ACC Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTG ACC TGC AAC GAC TAC ACC GCG ACC CAG GAG GAG TAC GAA GGC ACC Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACC TCT CGC AAC AGG GGT TAC GAC GGC GCC TAC GAG TCC AAC AGC Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCC GTG CCA GCC GAC TAC GCC AGC GCC TAC GAG GAG AAA GCC TAC ACC Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAC GGT AGA CGC GAC AAC CCA TGT GAG AGC AAC AGA GGC TAC GGC GAC Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACC CCC CTG CCC GCT GGA TAC GTG ACC AAG GAG CTG GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCC GAG ACC GAC AAG GTG TGG ATC GAG ATT GGC GAG ACC GAG GGC ACC Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAG CTG CTG ATG GAG GAG TAG Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1181 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile  
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile  
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
 370 375 380  
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 385 390 395 400  
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 405 410 415  
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
 420 425 430  
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 435 440 445  
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 450 455 460  
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 465 470 475 480  
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 485 490 495  
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
 500 505 510  
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
 515 520 525  
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 530 535 540  
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
 545 550 555 560  
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
 565 570 575  
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
 580 585 590  
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
 595 600 605  
 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
 610 615 620  
 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
 625 630 635 640  
 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
 645 650 655  
 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
 660 665 670  
 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 675 680 685  
 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr

690	695	700	
Asp Ile Thr Ile Gln Gly	Gly Asp Asp Val Phe Lys Glu Asn Tyr	Val	
705	710	715	720
Thr Leu Gln Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr	Leu Tyr Gln		
725	730	735	
Pro Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr	Gln Leu Arg		
740	745	750	
Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr	Leu Ile Arg Tyr		
755	760	765	
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr	Gly Ser Leu Trp		
770	775	780	
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly	Glu Pro Asn Arg		
785	790	795	800
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys	Ser Cys Arg		
805	810	815	
Asp Gly Glu Lys Cys Ala His His Ser His His	Phe Ser Leu Asp Ile		
820	825	830	
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly	Val Trp Val Ile		
835	840	845	
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly	Asn Leu Glu		
850	855	860	
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala	Arg Val Lys		
865	870	875	880
Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys	Leu Glu Trp Glu		
885	890	895	
Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp	Ala Leu Phe		
900	905	910	
Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr	Asn Ile Ala Met		
915	920	925	
Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg	Glu Ala Tyr Leu		
930	935	940	
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala	Ile Phe Glu Glu		
945	950	955	960
Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp	Ala Arg Asn		
965	970	975	
Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys	Trp Asn Val		
980	985	990	
Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His	Arg Ser Val Leu		
995	1000	1005	
Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val	Arg Val Cys		
1010	1015	1020	

SEQUENCE REPORT

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
 1025 1030 1035 1040  
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
 1045 1050 1055  
 Leu Lys Phe Ser Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr  
 1060 1065 1070  
 Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
 1075 1080 1085  
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
 1090 1095 1100  
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
 1105 1110 1115 1120  
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
 1125 1130 1135  
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
 1140 1145 1150  
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
 1155 1160 1165  
 Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3547 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..3543
  - (D) OTHER INFORMATION: /product= "Full-length, hybrid,  
maize optimized heat stable cryIA(b)"  
/note= "Disclosed in Figure 15 as contained in pCIB5514."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG  
 Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu  
 1185 1190 1195

48

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC  
 Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

96

1200	1205	1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215	1220	1225	144
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230	1235	1240	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250	1255	1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265	1270	1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280	1285	1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295	1300	1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310	1315	1320	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330	1335	1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345	1350	1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360	1365	1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375	1380	1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390	1395	1400	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410	1415	1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425	1430	1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440	1445	1450	816

CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455	1460	1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470	1475	1480	1485
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490	1495	1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505	1510	1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520	1525	1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535	1540	1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550	1555	1560	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570	1575	1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585	1590	1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600	1605	1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Val Ser Ile Ile 1615	1620	1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630	1635	1640	1645
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650	1655	1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665	1670	1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680	1685	1690	1536

GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695 1700 1705	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1710 1715 1720 1725	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1730 1735 1740	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1745 1750 1755	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 1760 1765 1770	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1775 1780 1785	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1790 1795 1800 1805	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1810 1815 1820	1920
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1825 1830 1835	1968
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1840 1845 1850	2016
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1855 1860 1865	2064
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 1870 1875 1880 1885	2112
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1890 1895 1900	2160
ACG CTA TTG GGT ACC TTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAA Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1905 1910 1915	2208
AAA ATA GAT GAG TCG AAA TTA AAA GCC TAT ACC CGT TAC CAA TTA AGA Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1920 1925 1930	2256
GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT CGC TAC	2304

BIOCHEMISTRY

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr		
1935	1940	1945
AAT GCC AAA CAC GAA ACA GTA AAT GTG CCA GGT ACG GGT TCC TTA TGG		2352
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp		
1950	1955	1960
1965		
CCG CTT TCA GCC CCA AGT CCA ATC GGC AAG TGC GGG GAG CCG AAT CGA		2400
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg		
1970	1975	1980
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG		2448
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg		
1985	1990	1995
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC TTC AGC CTG GAC ATC		2496
Asp Gly Glu Lys Cys Ala His His Ser His Phe Ser Leu Asp Ile		
2000	2005	2010
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC		2544
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile		
2015	2020	2025
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA		2592
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu		
2030	2035	2040
2045		
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA		2640
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys		
2050	2055	2060
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA		2688
Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu		
2065	2070	2075
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT		2736
Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe		
2080	2085	2090
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG		2784
Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met		
2095	2100	2105
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG		2832
Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu		
2110	2115	2120
2125		
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA		2880
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu		
2130	2135	2140
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT		2928
Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn		
2145	2150	2155
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG		2976
Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val		
2160	2165	2170
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT		3024
Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu		

2175	2180	2185						
GTT	GTT	CGT	TGT					
Val	Val	Pro	Glu					
2190	2195	2200	2205					
CCG	GGT	CGT	TAT					
Pro	Gly	Arg	ATC					
2210	2215	2220	3072					
GAA	GGC	CTT	CGT					
Gly	Tyr	CGT	ACA					
2225	2230	2235	3120					
TGC	GTA	ATT	GAC					
Gly	Gly	CAT	GAA					
2240	2245	2250	3168					
CTG	AAG	TTT	ACG					
Leu	Lys	AGC	AAC					
2255	2260	2265	3216					
GTA	ACG	TGT	AAT					
Val	Thr	GAT	TAT					
2270	2275	2280	3264					
TAC	ACT	TCT	CGT					
Tyr	Thr	Ser	Arg					
2290	2295	2300	3312					
TCT	GTA	CCA	GCT					
Ser	Val	Pro	Ala					
2305	2310	2315	3360					
GAT	GGA	CGA	AGA					
Asp	Gly	Arg	Asp					
2320	2325	2330	3408					
TAC	ACA	CCA	CTA					
Tyr	Thr	Pro	Leu					
2335	2340	2345	3456					
CCA	GAA	ACC	GAT					
Pro	Glu	Thr	Asp					
2350	2355	2360	3504					
TTC	ATC	GTG	GAC					
Phe	Ile	Val	Asp					
2350	2355	2360	3547					
GTG	GAA	TTA	CTT	ATG	GAG	GAA	TAAG	
Glu	Leu	Leu	Leu	Tyr	Asn	Cys	Leu	

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1															

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly  
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser  
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile  
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile  
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala  
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu  
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala  
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser  
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

340

345

350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
 370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
 385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
 405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
 420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
 435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
 450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
 465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
 485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
 500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
 515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
 530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
 545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
 565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
 580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
 595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
 610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
 625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
 645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
 660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 675 680 685  
 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
 690 695 700  
 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
 705 710 715 720  
 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
 725 730 735  
 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
 740 745 750  
 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
 755 760 765  
 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
 770 775 780  
 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg  
 785 790 795 800  
 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg  
 805 810 815  
 Asp Gly Glu Lys Cys Ala His His Ser His Phe Ser Leu Asp Ile  
 820 825 830  
 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
 835 840 845  
 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
 850 855 860  
 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys  
 865 870 875 880  
 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu  
 885 890 895  
 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
 900 905 910  
 Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
 915 920 925  
 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu  
 930 935 940  
 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
 945 950 955 960  
 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
 965 970 975  
 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val  
 980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
 995 1000 1005  
 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
 1010 1015 1020  
 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
 1025 1030 1035 1040  
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
 1045 1050 1055  
 Leu Lys Phe Ser Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr  
 1060 1065 1070  
 Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
 1075 1080 1085  
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
 1090 1095 1100  
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
 1105 1110 1115 1120  
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
 1125 1130 1135  
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
 1140 1145 1150  
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
 1155 1160 1165  
 Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu  
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4817 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794 ..2871, 3001..3135, 3236..3370)
    - (D) OTHER INFORMATION: /product= "maize TrpA"
- /note= "Maize TrpA sequence as disclosed in Figure 24."

- (ix) FEATURE:
  - (A) NAME/KEY: TATA\_signal
  - (B) LOCATION: 1594..1599

- (ix) FEATURE:

(A) NAME/KEY: CAAT\_signal  
(B) LOCATION: 1495..1499

(ix) FEATURE:

(A) NAME/KEY: promoter  
(B) LOCATION: 39..1838

(D) OTHER INFORMATION: /function= "Promoter sequence used  
in pCIB4433"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCGGAT CCATTAAGA AGTCTTGAA CAGATTCTAG AGATCTAGTT TAATGAGCTC	60
CACAAAAGTCT TGAAAAAATT CAGCGGGGAG GCCATTAGGG CAGGGGTACT GTTATGTTTT	120
AAAGAGAACCA CCACTTTCTT GATCTCTTCT AAAGAGAAAT GTTTGTAAG AAGGATCCTG	180
TCCTCCTCAT CCAACCTTTT CATCGGAAA TTTTCATAG AGATATTAGA GGCAAGAGAG	240
GGGCCAAAAA GATCCATGTA AATGGAAGTG GCCACCTGGT TGATACCTCC CTCATCTTCA	300
ACAGAAAATC CATTATGAAA AAGTGAATGG ATTTTAAACT CTTCTTTTC TTCCCTTTG	360
CAATGAGCTG AAAATATCTG GTATTATTCT CATCACCCCTC ATTAATGAAT CTGCCCCTAG	420
CAATTTGCTT TCTCTTGATC CCTCTGCAG CCACCATGTT TCTTAAATTC CACTCCATAT	480
CAAGCTTTTC CAATCTATCA GAATCTGAGA TGGCTGCAAT CTCTCTCATT TTCTCAAGGA	540
TATCGATGTT ATCCATAAGG TATTCTTGAA ACTTCTTATA TTTCCCTTCG ACATTTATAT	600
TCCATCCTTT CAACATTTTT TTGTTCAATC TTTTTGTTT TTTCCCTTTC CAAACATCGA	660
TACATTCCT GCTCCTCACCA GGTAAGGACG AGCTTCAAA AAACCTCTG CTTTAAAGTC	720
AGGTCTGAGC CTCCAGAAA GCTCACATAT CTAAAGTCCC TCTTCTTAGT TGGGACAGAG	780
TCAGTGCTAA GACACATGGG AACATGACCA GAAAAAAAAA ATCATATTAA GCCCAGAGAC	840
AACAATATTC TTGTACTGCA AGTCTCGTTA TGGGCTAGCA AAGGAATCTA CCCAACTTCT	900
CAAATGTGTT GGGATGTCAA GTATATAGAC TATTCTACAG TTCCAACCTCT ATCAAACATGT	960
GCAGCTCAAT TATAGAGTTG AATAAAAGTGC TCCATCTATT TGTTCTTATC CTCATATTG	1020
GTTAAGATAT TAAAATCACCA TCCCACCAAC ATTTAAAGTG CACCATTAA AGTGGCTCGC	1080
GAGCACCAAA CCGCTGAAAA CGGGAAATGT TTAGCACGTT GGCAGCGGGA CCCTTTCTA	1140
TCTCATCGTG TTCTCGTTG TCCACCACGG CCCACGGGCC AACGCTCCTC CATCCTGTAG	1200
TGTAGAGTAT ATTCCATTG CGACCGAGCC GAGCATCGAT CCAGCCACAC TGGCCACTGC	1260
CAGCCAGCCA TGTGGCACTC CTACGTATAC TACGTGAGGT GAGATTCACT CACATGGGAT	1320
GGGACCGAGA TATTTTACTG CTGTGGTTGT GTGAGAGATA ATAAAGCATT TATGACGATT	1380
GCTGAACAGC ACACACCAGT CGTCCAGATA GAGAAAGCTT TCTCTCTTA TTCGCATGCA	1440
TGTTTCATTA TCTTTATCA TATATATATA ACACATATTA AATGATTCTT CGTTCCAATT	1500

TATAATTCA	TTGACTTTT	TATCCACCGA	TGCTCGTTT	ATTAAAAAA	ATATTATAAT	1560
TATTGTTACT	TTTGTTGTA	ATATTGTTA	GCATATAATA	AACTTTGATA	CTAGTATGTT	1620
TCCGAGCAAA	AAAAAATATT	AATATTTAGA	TTACGAGCCC	ATTAATTAAT	TATATTGAG	1680
ACAAGCGAAG	CAAAGCAAAG	CAAGCTAATG	TTGCCCTGC	TGTGCATGCA	GAGGCCCGCT	1740
CTTGCTATAA	ACGAGGCAGC	TAGACCGGAC	TCGACTCATC	AGCCTCATCA	ACCTCGACGA	1800
AGGAGGAACG	AACGGACAGG	TTGTTGCACA	GAAGCGAC	ATG GCT TTC	GCG CCC	1853
			Met Ala Phe Ala Pro			
			1		5	
AAA ACG TCC	TCC TCC TCC	TCG CTG TCC	TCG GCG TTG	CAG GCA GCT CAG		1901
Lys Thr Ser	Ser Ser Ser	Ser Ser Leu	Ser Ser Ala	Leu Gln Ala Ala Gln		
10			15		20	
TCG CCG CCG	CTG CTC CTG	AGG CGG ATG TCG	TCG ACC GCA ACA CCG AGA			1949
Ser Pro Pro	Leu Leu Leu	Arg Arg Met	Ser Ser Thr Ala	Thr Pro Arg		
25			30		35	
CGG AGG TAC GAC	GCG GCC GTC GTC	ACT ACC ACC ACT GCT AGA				1997
Arg Arg Tyr Asp	Ala Ala Val	Val Val Thr	Thr Thr Ala	Arg		
40			45		50	
GCT GCG GCG	GCT GTC ACG GTT	CCC GCC CCG CCG CAG GCG GGC				2045
Ala Ala Ala	Ala Val Thr Val	Pro Ala Ala Pro Pro	Gln Ala Gly			
55			60		65	
CGC CGC CGC	CGG TGC CAC CAA	AGC AAG CGG CGG CAC CCG CAG AGG AGG				2093
Arg Arg Arg	Arg Cys His Gln Ser	Lys Arg Arg His Pro Gln Arg Arg				
70			75		80	
AGC CGT CCG	GTG TCG GAC ACC ATG GCG GCG	CTC ATG GCC AAG GGC AAG				2141
Ser Arg Pro	Val Ser Asp Thr Met	Ala Ala Leu Met Ala Lys Gly Lys				
90			95		100	
GTTCGTATAG	TACGCGCGCG	TGTCGTCGTC	GTTATTTGC	GCATAGGCAC	GGACATACAC	2201
GTGCTTAGC	TAGCTAACAG	CTAGATCATC	GGTGCAG ACG GCG	TTC ATC CCG TAC		2256
			Thr Ala Phe Ile Pro Tyr			
			105			
ATC ACC GCC	GGC GAC CCG GAC	CTA GCG ACG ACG	GCC GAG GCG CTG CGT			2304
Ile Thr Ala	Gly Asp Pro Asp	Leu Ala Thr Thr	Ala Glu Ala Leu Arg			
110			115		120	
CTG CTG GAC	GGC TGT GGC	GAC GTC ATC GAG CTG GGG GTA	CCC TGC			2352
Leu Leu Asp	Gly Cys Gly	Ala Asp Val Ile	Glu Leu Gly Val Pro Cys			
125			130		135	
TCG GAC CCC	TAC ATC GAC	GGG CCC ATC ATC CAG	GCG TCG GTG GCG CGG			2400
Ser Asp Pro	Tyr Ile Asp Gly	Pro Ile Ile	Gln Ala Ser Val Ala Arg			
140			145		150	
GCT CTG GCC	AGC GGC ACC ACC	ATG GAC GCG GTG CTG	GAG ATG CTG AGG			2448
Ala Leu Ala	Ser Gly Thr Thr	Met Asp Ala Val Leu Glu Met	Leu Leu Arg			
160			165		170	

GAG GTG ACG CCG GAG CTG TCG TGC CCC GTG GTG CTC CTC TCC TAC TAC Glu Val Thr Pro Glu Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr 175 180 185	2496
AAG CCC ATC ATG TCT CGC AGC TTG GCC GAG ATG AAA GAG GCG GGG GTC Lys Pro Ile Met Ser Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val 190 195 200	2544
CAC GGTAACATA GCTAGCTCTT CCGATCCCC TTCAATTAAAT TAATTTATAG His	2597
TAGTCCATTC ATGTGATGAT TTTTGTTTTT CTTTTTACTG ACA GGT CTT ATA GTG Gly Leu Ile Val 205	2652
CCT GAT CTC CCG TAC GTG GCC GCG CAC TCG CTG TGG AGT GAA GCC AAG Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 215 220	2700
AAC AAC AAC CTG GAG CTG GTAGGTTGAA TTAAGTTGAT GCATGTGATG Asn Asn Asn Leu Glu Leu 225 230	2748
ATTTATGTAG CTAGATCGAG CTAGCTATAA TTAGGAGCAT ATCAG GTG CTG CTG Val Leu Leu	2802
ACA ACA CCA GCC ATA CCA GAA GAC AGG ATG AAG GAG ATC ACC AAG GCT Thr Thr Pro Ala Ile Pro Glu Asp Arg Met Lys Glu Ile Thr Lys Ala 235 240 245	2850
TCA GAA GGC TTC GTC TAC CTG GTAGTTATAT GTATATATAG ATGGACGACG Ser Glu Gly Phe Val Tyr Leu 250 255	2901
TAACTCATTC CAGCCCCATG CATATATGGA GGCTTCATT CTGCAGAGAC GACGAAGACC	2961
ACGACGACGA CTAACACTAG CTAGGGCGT ACGTTGCAG GTG AGC GTG AAC GGA Val Ser Val Asn Gly 260	3015
GTG ACA GGT CCT CGC GCA AAC GTG AAC CCA CGA GTG GAG TCA CTC ATC Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg Val Glu Ser Leu Ile 265 270 275	3063
CAG GAG GTT AAG AAG GTG ACT AAC AAG CCC GTT GCT GTT GGC TTC GGC Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val Ala Val Gly Phe Gly 280 285 290	3111
ATA TCC AAG CCC GAG CAC GTG AAG CAGGTACGTA CGTAGCTGAC CAAAAAAAAC Ile Ser Lys Pro Glu His Val Lys 295 300	3165
TGTTAACAAAG TTTTGTGGA CAAGCCGGCT ACTAGCTAGC TAACAGTGAT CAGTGACACA	3225
CACACACACA CAG ATT GCG CAG TGG GGC GCT GAC GGG GTG ATC ATC GGC Gln Ile Ala Gln Trp Gly Ala Asp Gly Val Ile Ile Gly 305 310	3274
AGC GCC ATG GTG AGG CAG CTG GGC GAA GCG GCT TCT CCC AAG CAA GGC	3322

Ser Ala Met Val Arg Gln Leu Gly Glu Ala Ala Ser Pro Lys Gln Gly  
 315 320 325 330  
 CTG AGG AGG CTG GAG GAG TAT GCC AGG GGC ATG AAG AAC GCG CTG CCA 3370  
 Leu Arg Arg Leu Glu Glu Tyr Ala Arg Gly Met Lys Asn Ala Leu Pro  
 335 340 345  
 TGAGTCCATG ACAAAAGTAAA ACGTACAGAG ACACATTGATA ATATCTATCT ATCATCTCGG 3430  
 AGAAGACGAC CGACCAATAA AAATAGCCA AGTGGAACTG AAGCTTAGCT GTATATACAC 3490  
 CGTACGTCGT CGTCGTCGTT CCGGATCGAT CTCGGCCGGC TAGCTAGCAG AACGTGTACG 3550  
 TAGTAGTATG TAATGCATGG AGTGTGGAGC TACTAGCTAG CTGGCCGTT ATTGATTAT 3610  
 AATTCTTCGC TCTGCTGTGG TAGCAGATGT ACCTAGTCGA TCTTGTACGA CGAAGAAGCT 3670  
 GGCTAGCTAG CCGTCTCGAT CGTATATGTA CTGATTAATC TGCAGATTGA ATAAAAACTA 3730  
 CAGTACGCAT ATGATGCGTA CGTACGTGTG TATAGTTGT GCTCATATAT GCTCCTCATC 3790  
 ACCTGCCTGA TCTGCCCATC GATCTCTCTC GTACTCCTTC CTGTTAAATG CCTTCTTTGA 3850  
 CAGACACACC ACCACCAAGCA GCAGTGACGC TCTGCACGCC GCCGCTTAA GACATGTAAG 3910  
 ATATTTTAAG AGGTATAAGA TACCAAGGAG CACAAATCTG GAGCACTGGG ATATTGCAAA 3970  
 GACAAAAAAA AAACAAAATT AAAGTCCCAC CAAAGTAGAG ATAGTAAAGA GGTGGATGGA 4030  
 TTAAAATTAT CTCATGATTT TTGGATCTGC TCAAATAGAT CGATATGGTA TTCAGATCTA 4090  
 TGTTGTATAG CCTTTTCATT AGCTTTCTGA AAAAAAAATG GTATGATGAG TGCGGAGTAG 4150  
 CTAGGGCTGT GAAGGAGTCG GATGGGCTTC CACGTACTTG TTTGTGGCC TAGTCCGGTT 4210  
 CTATTTAGGT CCGATCCGAG TCCGGCATGG TCCGGTTCCA TACGGGCTAG GACCAAGCTC 4270  
 GCCACGTGAG TTTAGGCCG GTCGGCTAGC CCGAGCACGA CCCGTTTTA AACTGGCTAG 4330  
 GACTCGCCCA TTTAATAAGA CAAACATTGC AAAAAATAGC TCTATTTTT ATTAAAATA 4390  
 TATTGTTTAT TTGTGAAATG TGTATTATTT GTAATATATA TTATTGTATA TAGTTATATC 4450  
 TTCAATTATG ATTTATAAAAT ATGTTTTTA TTATGAACTC AATTTTAAGT TTGATTTATG 4510  
 CGTTGGCGGG CTCGAGGAGG CACGGTGAAC ATTTTGCGGT CGGGCTTAAC GGGTCGGCCC 4570  
 GGCCCCGGTTC GGCCCATCCA CGGCCCATCC CGTGTGGCC TCGTTGGTG AGTCAGCCC 4630  
 GTCGGACAAC CCGTCCCCGG CCCGGATAAT TAATCGGGCC TAACCGTGGC GTGCTTAAAC 4690  
 GGTCCGTGCC TCAACGGACC GGGCCGGGG CGGGCCGTTT GACATCTCTA GTGGTGTGAT 4750  
 TAGAGATGGC GATGGGAACC GATCACTGAT TCCGTGTGGA GAATTCGATA TCAAGCTTAT 4810  
 CGATACC 4817

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala  
1 5 10 15

Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser  
20 25 30

Thr Ala Thr Pro Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr  
35 40 45

Thr Thr Thr Ala Arg Ala Ala Ala Ala Val Thr Val Pro Ala Ala  
50 55 60

Pro Pro Gln Ala Gly Arg Arg Arg Cys His Gln Ser Lys Arg Arg  
65 70 75 80

His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu  
85 90 95

Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp  
100 105 110

Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys  
115 120 125

Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile  
130 135 140

Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly  
145 150 155 160

Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu  
165 170 175

Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser  
180 185 190

Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val  
195 200 205

Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys  
210 215 220

Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu  
225 230 235 240

Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu  
245 250 255

Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg  
260 265 270

Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val  
275 280 285

Ala Val Gly Phe Gly Ile Ser Lys Pro Glu His Val Lys Gln Ile Ala  
 290 295 300  
 Gln Trp Gly Ala Asp Gly Val Ile Ile Gly Ser Ala Met Val Arg Gln  
 305 310 315 320  
 Leu Gly Glu Ala Ala Ser Pro Lys Gln Gly Leu Arg Arg Leu Glu Glu  
 325 330 335  
 Tyr Ala Arg Gly Met Lys Asn Ala Leu Pro  
 340 345

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 3..1226  
 (D) OTHER INFORMATION: /note= "cDNA sequence for maize  
 pollen-specific calcium dependent protein kinase gene as  
 disclosed in Figure 30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC	47
Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu	
350 355 360	
CGC GGC GCG TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG	95
Arg Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu	
365 370 375	
TGC GCG GGC GGG GAG CTC TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC	143
Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr	
380 385 390	
ACG GAG CGC GGC GCC GCG GAG CTG CTG CGC GCC ATC GTG CAG ATC GTG	191
Thr Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val	
395 400 405	
CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC ATC AAG CCC GAG	239
His Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu	
410 415 420 425	
AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC ACC	287
Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr	
430 435 440	
GAC TTC GGC CTC TCC GTC TTC AAG GAG GGC GAG CTG CTC AGG GAC	335

50

Asp Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp		
445	450	455
ATC GTC GGC AGC GCC TAC TAC ATC GCG CCC GAG GTG CTC AAG AGG AAG		383
Ile Val Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys		
460	465	470
TAC GGC CCG GAG GCC GAC ATC TGG AGC GTC GGC GTC ATG CTC TAC ATC		431
Tyr Gly Pro Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile		
475	480	485
TTC CTC GCC GGC GTG CCT CCC TTC TGG GCA GAG AAC GAG AAC GGC ATC		479
Phe Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile		
490	495	500
505		
TTC ACC GCC ATC CTG CGA GGG CAG CTT GAC CTC TCC AGC GAG CCA TGG		527
Phe Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp		
510	515	520
CCA CAC ATC TCG CCG GGA GCC AAG GAT CTC GTC AAG AAG ATG CTC AAC		575
Pro His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn		
525	530	535
ATC AAC CCC AAG GAG CGG CTC ACG GCG TTC CAG GTC CTC AAT CAC CCA		623
Ile Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro		
540	545	550
TGG ATC AAA GAA GAC GGA GAC GCG CCT GAC ACG CCG CTT GAC AAC GTT		671
Trp Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val		
555	560	565
GTT CTC GAC AGG CTC AAG CAG TTC AGG GCC ATG AAC CAG TTC AAG AAA		719
Val Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys		
570	575	580
585		
GCA GCA TTG AGG ATC ATA GCT GGG TGC CTA TCC GAA GAG GAG ATC ACA		767
Ala Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr		
590	595	600
GGG CTG AAG GAG ATG TTC AAG AAC ATT GAC AAG GAT AAC AGC GGG ACC		815
Gly Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr		
605	610	615
ATT ACC CTC GAC GAG CTC AAA CAC GGG TTG GCA AAG CAC GGG CCC AAG		863
Ile Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys		
620	625	630
CTG TCA GAC AGC GAA ATG GAG AAA CTA ATG GAA GCA GCT GAC GCT GAC		911
Leu Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp		
635	640	645
GGC AAC GGG TTA ATT GAC TAC GAC GAA TTC GTC ACC GCA ACA GTG CAT		959
Gly Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His		
650	655	660
665		
ATG AAC AAA CTG GAT AGA GAA GAG CAC CTT TAC ACA GCA TTC CAG TAT		1007
Met Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr		
670	675	680
TTC GAC AAG GAC AAC AGC GGG TAC ATT ACT AAA GAA GAG CTT GAG CAC		1055
Phe Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His		

685	690	695	
GCC TTG AAG GAG CAA GGG TTG TAT GAC GCC GAT AAA ATC AAA GAC ATC Ala Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile 700	705	710	1103
ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA GAT TAT TCA GAG Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu 715	720	725	1151
TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG AAC Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn 730	735	740	1199
ATC AAG AAG AGG CGA GAC ATA GTC CTA TAGTGAAGTG AAGCAGCAAG Ile Lys Lys Arg Arg Asp Ile Val Leu 750			1246
TGTGTAATGT AATGTGTATA GCAGCTAAA CAAGCAAATT TGTACATCTG TACACAAATG			1306
CAATGGGGTT ACTTTGCAA AAAAAAAA AAAAAAAA AAA			1349

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 408 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg 1 5 10 15	
Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys 20 25 30	
Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr 35 40 45	
Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His 50 55 60	
Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn 65 70 75 80	
Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp 85 90 95	
Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Leu Leu Arg Asp Ile 100 105 110	
Val Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr 115 120 125	
Gly Pro Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe 130 135 140	

Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe  
 145 150 155 160  
 Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro  
 165 170 175  
 His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile  
 180 185 190  
 Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp  
 195 200 205  
 Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val  
 210 215 220  
 Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala  
 225 230 235 240  
 Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly  
 245 250 255  
 Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile  
 260 265 270  
 Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu  
 275 280 285  
 Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly  
 290 295 300  
 Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met  
 305 310 315 320  
 Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe  
 325 330 335  
 Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala  
 340 345 350  
 Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile  
 355 360 365  
 Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe  
 370 375 380  
 Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile  
 385 390 395 400  
 Lys Lys Arg Arg Asp Ile Val Leu  
 405

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 464 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..464

(D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly  
1 5 10 15

Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His  
20 25 30

Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys  
35 40 45

Leu Ala Ala Arg Glu Asp Val Asp Asp Val Arg Arg Glu Val Gln Ile  
50 55 60

Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala  
65 70 75 80

Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly  
85 90 95

Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg  
100 105 110

Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys  
115 120 125

His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu  
130 135 140

Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly  
145 150 155 160

Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly  
165 170 175

Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro  
180 185 190

Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala  
195 200 205

Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala  
210 215 220

Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile  
225 230 235 240

Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro  
245 250 255

Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys

260

265

270

Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp  
 275 280 285

Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu  
 290 295 300

Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Ile Thr Gly Leu Lys  
 305 310 315 320

Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile Thr Leu  
 325 330 335

Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu Ser Asp  
 340 345 350

Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly Asn Gly  
 355 360 365

Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys  
 370 375 380

Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys  
 385 390 395 400

Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys  
 405 410 415

Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp  
 420 425 430

Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe Val Ala  
 435 440 445

Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile Lys Lys  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: /note= "rat protein kinase II protein sequence as shown in Figure 32."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg  
 1 5 10 15

Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile  
 20 25 30

Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu  
 35 40 45

Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His  
 50 55 60

Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val  
 65 70 75 80

Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser  
 85 90 95

Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn  
 100 105 110

His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn  
 - 115 120 125

Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp  
 130 135 140

Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly  
 145 150 155 160

Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp  
 165 170 175

Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr  
 180 185 190

Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys  
 195 200 205

Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu  
 210 215 220

Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu  
 225 230 235 240

Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His  
 245 250 255

Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln  
 260 265 270

Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys  
 275 280 285

Gly Ala Ile Leu Thr Thr Met  
 290 295

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 142 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: /note= "human calmodulin protein sequence as shown in Figure 33."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe  
1 5 10 15

Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val  
20 25 30

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met  
35 40 45

Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu  
50 55 60

Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu  
65 70 75 80

Glu Ile Arg Glu Ala Phe Arg Val Lys Asp Lys Asp Gly Asn Gly Tyr  
85 90 95

Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys  
100 105 110

Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp  
115 120 125

Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met  
130 135 140

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..463

(D) OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val Leu Pro Gln Arg Thr Gln Asn Ile Arg Glu Val Tyr Glu Val Gly  
1 5 10 15

Arg Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Phe Glu Cys Thr Arg  
20 25 30

Arg Ala Ser Gly Gly Lys Phe Ala Cys Lys Ser Ile Pro Lys Arg Lys  
35 40 45

Leu Leu Cys Lys Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile  
50 55 60

Met His His Leu Ser Glu His Ala Asn Val Val Arg Ile Glu Gly Thr  
65 70 75 80

Tyr Glu Asp Ser Thr Ala Val His Leu Val Met Glu Leu Cys Glu Gly  
85 90 95

Gly Glu Leu Phe Asp Arg Ile Val Gln Lys Gly His Tyr Ser Glu Arg  
100 105 110

Gln Ala Ala Arg Leu Ile Lys Thr Ile Val Glu Val Val Glu Ala Cys  
115 120 125

His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu  
130 135 140

Phe Asp Thr Ile Asp Glu Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly  
145 150 155 160

Leu Ser Val Phe Tyr Lys Pro Gly Glu Ser Phe Cys Asp Val Val Gly  
165 170 175

Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu Arg Lys Leu Tyr Gly Pro  
180 185 190

Glu Ser Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser  
195 200 205

Gly Val Pro Pro Phe Trp Ala Glu Ser Glu Pro Gly Ile Phe Arg Gln  
210 215 220

Ile Leu Leu Gly Lys Leu Asp Phe His Ser Glu Pro Trp Pro Ser Ile  
225 230 235 240

Ser Asp Ser Ala Lys Asp Leu Ile Arg Lys Met Leu Asp Gln Asn Pro  
245 250 255

Lys Thr Arg Leu Thr Ala His Glu Val Leu Arg His Pro Trp Ile Val  
260 265 270

Asp Asp Asn Ile Ala Pro Asp Lys Pro Leu Asp Ser Ala Val Leu Ser  
275 280 285

Arg Leu Lys Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala Leu

290	295	300
Arg Val Ile Ala Glu Arg Leu Ser Glu Glu Glu Ile Gly Gly Leu Lys		
305	310	315
Glu Leu Phe Lys Met Ile Asp Thr Asp Asn Ser Gly Thr Ile Thr Phe		
325	330	335
Asp Glu Leu Lys Asp Gly Leu Lys Arg Val Gly Ser Glu Leu Met Glu		
340	345	350
Ser Glu Ile Lys Asp Leu Met Asp Ala Ala Asp Ile Asp Lys Ser Gly		
355	360	365
Thr Ile Asp Tyr Gly Glu Phe Ile Ala Ala Thr Val His Leu Asn Lys		
370	375	380
Leu Glu Arg Glu Glu Asn Leu Val Ser Ala Phe Ser Tyr Phe Asp Lys		
385	390	395
Asp Gly Ser Gly Tyr Ile Thr Leu Asp Glu Ile Gln Gln Ala Cys Lys		
405	410	415
Asp Phe Gly Leu Asp Asp Ile His Ile Asp Asp Met Ile Lys Glu Ile		
420	425	430
Asp Gln Asp Asn Asp Gly Gln Ile Asp Tyr Gly Glu Phe Ala Ala Met		
435	440	445
Met Arg Lys Gly Asn Gly Gly Ile Gly Arg Arg Thr Met Arg Lys		
450	455	460

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1418..1427
  - (D) OTHER INFORMATION: /note= "start of mRNA"
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1481..2366
- (ix) FEATURE:
  - (A) NAME/KEY: intron
  - (B) LOCATION: 2367..2451
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 2452..2602

- (ix) FEATURE:  
(A) NAME/KEY: intron  
(B) LOCATION: 2603..2690
- (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION: 2691..2804
- (ix) FEATURE:  
(A) NAME/KEY: intron  
(B) LOCATION: 2805..2906
- (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION: 2907..3075
- (ix) FEATURE:  
(A) NAME/KEY: intron  
(B) LOCATION: 3076..3177
- (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION: 3178..3304
- (ix) FEATURE:  
(A) NAME/KEY: intron  
(B) LOCATION: 3305..3398
- (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION: 3399..3498
- (ix) FEATURE:  
(A) NAME/KEY: intron  
(B) LOCATION: 3499..3713
- (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION: 3714..3811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTAGTAACAC CTCTCCAATC GCTTGGGTTG GCACATTCTT AGCTTTATC ACATTTAAG	60
AAATAGAGTT CACCACCTTC AAAATAATGC CTATACAATG AATGATCGCT TGGATGCAAT	120
ATAGCTAGAT TCAACTAGCT ATATATGGTC AATAGAACCC TGTGAGCACC TCACAAACAC	180
GACTTCAATT TTGAGACCCCT AAGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA	240
GGACTTCTCC TTGCTAAATG CTTGTCAGCG ATCTATATAT CTTCCCCACT GCGGGAGATA	300
CTATATATAG GGCCTTGGAC CTCTAGGGTA TCTCAAAGGC CTAGTCACAA CAATTCTCAA	360
CAGTATTAA TTTTATACAT GTATGAACAG TGAGGAATT TGAGTGCCCA ACCCAAGAGT	420
GGGAGGTGTA AATTGGGTAG CTAAACTAA ATAGGGCTCT TCTTATTTAG GTTTATCTAG	480
TCTCTACTTA GACTAATTCA GAAAGAATT TACAACCTAT GGTTAACAT ATCTCTAGTC	540

TAAGCAAATT TAGGAAAGTT AAAAGCACAC AATTAGGCAC ATGTGAAAGA TGTGTATGGT 600  
 AAGTAAAAGA CTTATAAGGA AAAAGTGGGT GAATCCTCAA GATGTGGTGG TATATCCCAA 660  
 TGATATTAGA TGCCAGAATA TAGGGGGAA ATCGATGTAT ACCATCTCTA CCAGGATACC 720  
 TGTGCGGACT GTGCACTGA CACATGGACC ATGGTGTCTT CTTAGATTG GTTATTAGCT 780  
 AATTGCGCTA CAACTGTTC AAGGCTAGAC CAAATTAAAA AACTAATATT AAACATAAAA 840  
 AGTTAGGCAA ACTATAGTAA ATTATGCAGC GATCCAACAA CAAGCCATGT CTCGTGGTC 900  
 ATGAGCCACG CGTCGCCAT ACACCCACAT GATGTTCCA TACGGATGGT CCTTATGCAA 960  
 TTTTGTCTGC AAAACACAAG CCTTAATACA GCCACGCGAC AATCATGGAA GTGGTCGTTT 1020  
 TAGGTCTCA TCATGAAGTT CAGGGAAAAC GCATCAAATG TAATGCAGAG AAATGGTATT 1080  
 TCTTCTCTTG TAAATCAGGG AGAGGAGTAC CATCACTACA GATTCAAGAT CAGAATTCA 1140  
 TCTTCCAACG ACAATAATCG CAGCATTG TAAAAATTG CAGAAACTTC TGTTGACTT 1200  
 GTAGCCCTGA CCTTGCAAA TATTTGAAGT TGTGCCTGCT GACACAACCTT CAATCTGGAA 1260  
 GTGCTGTTGA TCAGTMTTGC CAGAACAGC AAGCAGCCTA TATATATCTG TCACGAGACA 1320  
 CCCTGCCGCC CTCTTCTTTC CCGCCATTCC CTCCCTACCC TTCAAAATCT AGAAACCTTT 1380  
 TTTTTCTTC CCGATACGCC CCTCCATCTC TCGCCGTTCA TGTCCGTGGC TGGCTGCCCT 1440  
 CCGTGGGAGC AGGGGGCCGC ACTCGTTCCC CGCCGCAGCC ATGGGCCAGT GCTGCTCCAA 1500  
 GGGCGCCGGA GAGGCCCGC CACCGAGGCG CCAAACGGCA GGCGCCAAGC CGCGGGCGTC 1560  
 CGCGAACAAAC GCCGACGGAC AACGGGGCGTC GTCCTCGTCC GCGGTGGCTG CTGCCGCTGC 1620  
 TGCTGCCGGT GGTGGTGGCG GCGGCACGAC GAAGCCGGCC TCACCCACCG GCGGCGCCAG 1680  
 GGCCAGCTCC GGCAGCAAAC CGGCAGCCGC CGTGGGCACG GTGCTGGCC GGCCATGGA 1740  
 GGACGTGCCGC GCGACCTACT CGATGGCAA GGAGCTCGGG CGCGGGCAGT TCGGCGTGAC 1800  
 GCACCTGTGC ACGCACCGGA CGAGCGCGA GAAGCTGGCG TGCAAGACGA TCGCGAAGCG 1860  
 GAAGCTGGCG GCCAGGGAGG ACGTGGACGA CGTGCAGCGG GAGGTGCAGA TCATGCACCA 1920  
 CCTCTCCGGC CAGCCCAACG TGGTGGCCT CCGCGCGCG TACGAGGACA AGCAGAGCGT 1980  
 GCACCTCGTC ATGGAGCTGT GCGCGGGCGG GGAGCTCTTC GACCGCATCA TCGCCCGGGG 2040  
 CCAGTACACG GAGCGCGCG CCGCGGAGCT GCTGCGCGCC ATCGTGCAGA TCGTGCACAC 2100  
 CTGCCACTCC ATGGGGGTGA TGCACCGGG CATCAAGCCC GAGAACTTCC TGCTGCTCAG 2160  
 CAAGGACGAG GACCGCCGC TCAAGGCCAC CGACTTCGGC CTCTCCGTCT TCTTCAAGGA 2220  
 GGGCGAGCTG CTCAGGGACA TCGTCGGCAG CGCCTACTAC ATCGCGCCCG AGGTGCTCAA 2280  
 GAGGAAGTAC GGCGGGAGG CCGACATCTG GAGCGTCGGC GTCATGCTCT ACATCTTCCT 2340

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CGCCGGCGTG CCTCCCTTCT GGGCAGGTCTG GATCCGTCCG TGTCGTCT AGACGATATA	2400
CAGAACCCGA CGATGGATTT GCTTCTCAGC CCTGTTCTTG CATCACCAAGA GAACGAGAAC	2460
GGCATCTTCA CCGCCATCCT GCGAGGGCAG CTTGACCTCT CCAGCGAGCC ATGGCCACAC	2520
ATCTCGCCGG GAGCCAAGGA TCTCGTCAAG AAGATGCTCA ACATCAACCC CAAGGAGCGG	2580
CTCACGGCGT TCCAGGTCTT CAGTAAGTAC CCAGATCGTT GCTGTCATAC ACTCATATGA	2640
ATTGTATCGT TCATGAGCAA CGATCGAGCG GATTTGGTGA ACTTGTAGAT CACCCATGGA	2700
TCAAAGAAGA CGGAGACGCG CCTGACACGC CGCTTGACAA CGTTGTTCTC GACAGGCTCA	2760
AGCAGTTCAAG GGCCATGAAC CAGTTCAAGA AAGCAGCATT GAGGGTACAT TATCTGATAA	2820
AAGCTCCACA AATACAACCTT CTGAAGAACAA GCAATGCTTA CACGGCAGAA TTTTCATTAT	2880
AAATGCTCTT GATGACATAA TGTTAGATCA TAGCTGGGTG CCTATCCGAA GAGGAGATCA	2940
CAGGGCTGAA GGAGATGTTA AAGAACATTG ACAAGGATAA CAGCGGGACC ATTACCCCTCG	3000
ACGAGCTCAA ACACGGGTTG GCAAAGCAGC GGCCCAGCT GTCAGACAGC GAAATGGAGA	3060
AACTAATGGA AGCAGTGAGT TTTCAGAGTA CAATCTAAA AAAAGGAATT GTGATTCTTT	3120
TCAAAATGAA GAAGTAATCT GAAAACATCC CTGCTGAAAT GCTTTATACA TTTCCAGGCT	3180
GACGCTGACG GCAACGGGTT AATTGACTAC GACGAATTG TCACCGCAAC AGTGCATATG	3240
AACAAACTGG ATAGAGAAGA GCACCTTAC ACAGCATTCC AGTATTCGA CAAGGACAAC	3300
AGCGGGTAAG TTGAACGTTA AAATGATACA GCTGGTACCT GAATTCTGGA CAACACATAT	3360
CATAACAGGA CACATATATA ATTCTGTTAT CTCACAGGTA CATTACTAAA GAAGAGCTTG	3420
AGCACGCCTT GAAGGAGCAA GGGTTGTATG ACGCCGATAA AATCAAAGAC ATCATCTCG	3480
ATGCCGACTC TGACAATGTA AGGAACAAAC ATTATTTAAA TTTCAGCCGA CAAACTAAAC	3540
TATAGAAACC ACATCATGAT ATCAAATTGAGGTTGGCGG TGCTACAGAA ATAGAACCCA	3600
GTACACCAAA ATGACTAACT TGTCTGATT AGTTGTTCT CGTAACTGAA CATTGTTGTT	3660
CTTAGTTCT TATTGTTAAA CCAAAGACTT AAATTCACCT TTGCACATGC AGGATGGAAG	3720
GATAGATTAT TCAGAGTTG TGGCGATGAT GAGGAAAGGG ACGGCTGGTG CCGAGCCAAT	3780
GAACATCAAG AAGAGGCGAG ACATAGTCCT ATAGTGAAGT GAAGCAGAAG TGTGTAATGT	3840
AATGTGTATA GCAGCTCAA CAAGCAAATT TGTACATCTG TACACAAATG CAATGGGGTT	3900
ACTTTGCAA CTTAGTTCAT GGATGGTTGT GTACGTTGTG CTATTGATTG CAAGTGATTT	3960
GAAAGACATG CATACTTAGG AACTGAGAAA GATAGATCTA CTACTGCTAG AGACAGAACAA	4020
ATAGGATAAT TCAGAAGTGG TATTCAGAA GACTACAGCT GGCATCTATT ATTCTCATTG	4080
TCCTCGCAA AATACTGATG ATGCATTGAGA GAGAACATAA TGCAACAAGA TCGAGCTCCC	4140
TATAGTGAGT CGTATTAGGC CA	4162

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)"  
/note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
410 415 420	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
425 430 435 440	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
445 450 455	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
460 465 470	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
475 480 485	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
490 495 500	
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
505 510 515 520	
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
525 530 535	
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
540 545 550	

ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 555 560 565	480
TAC GTG CAG GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 570 575 580	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 585 590 595 600	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 605 610 615	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 620 625 630	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 635 640 645	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 650 655 660	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 665 670 675 680	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 685 690 695	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 700 705 710	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 715 720 725	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 730 735 740	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 745 750 755 760	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 765 770 775	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 780 785 790	1152

GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 795 800 805	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 810 815 820	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 825 830 835 840	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 845 850 855	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 860 865 870	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 875 880 885	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 890 895 900	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 905 910 915 920	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 925 930 935	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 940 945 950	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 955 960 965	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 970 975 980	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 985 990 995 1000	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1005 1010 1015	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1020 1025 1030	1872
AAC GAG CTG TTC ACC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	1920

REVERSE TRANSLATION

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val		
1035	1040	1045
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT		1968
Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser		
1050	1055	1060
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA		2016
Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys		
1065	1070	1075
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC		2064
His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn		
1085	1090	1095
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG		2112
Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr		
1100	1105	1110
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT		2160
Asp Ile Thr Ile Gln Gly Asp Asp Val Phe Lys Glu Asn Tyr Val		
1115	1120	1125
ACG CTA TTG GGT ACC TTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAA		2208
Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln		
1130	1135	1140
AAA ATA GAT GAG TCG AAA TTA AAA GCC TAT ACC CGT TAC CAA TTA AGA		2256
Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg		
1145	1150	1155
1160		
GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT CGC TAC		2304
Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr		
1165	1170	1175
AAT GCC AAA CAC GAA ACA GCA AAT GTG CCA GGT ACG GGT TCC TTA TGG		2352
Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp		
1180	1185	1190
CCG CTT TCA GCC CCA AGT CCA ATC GGA AAA TGT GGG GAG CCG AAT CGA		2400
Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg		
1195	1200	1205
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG		2448
Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg		
1210	1215	1220
GAC GGG GAG AAG TGC GCC CAT CAT TCC CAT CAT TTC TCC TTG GAC ATT		2496
Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile		
1225	1230	1235
1240		
GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA GGT GTA TGG GTG ATA		2544
Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile		
1245	1250	1255
TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA AGA CTA GGA AAT CTA GAA		2592
Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu		
1260	1265	1270
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA		2640
Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys		

1275	1280	1285	
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 1290	1295	1300	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Ser Val Asp Ala Leu Phe 1305	1310	1315	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 1325	1330	1335	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 1340	1345	1350	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 1355	1360	1365	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 1370	1375	1380	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 1385	1390	1395	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 1405	1410	1415	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1420	1425	1430	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1435	1440	1445	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1450	1455	1460	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Val Tyr Pro Asn Asn Thr 1465	1470	1475	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1485	1490	1495	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1500	1505	1510	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1515	1520	1525	3360

GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1530 1535 1540	3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1545 1550 1555 1560	3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1565 1570 1575	3504
TTC ATC GTG GAC GTG GAA TTA CTT CTT ATG GAG GAA TAA Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1580 1585	3546

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg  
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val  
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg  
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val  
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro  
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu  
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr  
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln  
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro  
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala  
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg  
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp  
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val  
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln  
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His  
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile  
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn  
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr  
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly  
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg  
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg  
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg  
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn  
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn  
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu  
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val  
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val  
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser  
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys  
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr  
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
770 775 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg  
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg  
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile

820

825

830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
 835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
 850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys  
 865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu  
 885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
 900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
 915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu  
 930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
 945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
 965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val  
 980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
 995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
 1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr  
 1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu  
 1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr  
 1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr  
 1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser  
 1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr  
 1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp  
 1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe  
 1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr  
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu  
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE74A28"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCAGATCTGG ATCCATGCAC GCCGTGAAGG GCCCTTCTAG AAGGCCTATC GATAAAGAGC 60  
TCCCCGGGGA TGGATTGCAC GCAGGTTTC 88

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE72A28"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCGTTAACAT GTCGACTCAG AAGAACTCGT CAAGAAGGCG 40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer P1(a)"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGACAAGG ATCCAACAAT GG

22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P1(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AATTGTCGAC AAGGATCCAA CAATGG

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P2(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACACGCTGAC GTCGGCGAGC ACG

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P2(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCTACACGC TGACGTCGCG CAG

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer A1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATTGTCGAC

10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer A2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGTGTAGCT

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P3(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCTGCGCGAC GTCAGCGTGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P3(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATTGCTGCG CGACGTCAGC GTG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCGTTGCCCGCC ATGGTGCCGT ACAGG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCTGGCGTT GCCCATGGTG CCG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer B1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATTGCTGCG

10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer B2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AACGCCAGCT

10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer P5(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCCCCTGT ACGGCACCAT GGGCAACGCC GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P5(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTGTACGG CACCATGGGC AAC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P6(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAGCCGGGG CCCTTCACCA CGCTGG

26

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer P6(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

210

AGCTGAAGCC GGGGCCCTTC ACC

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C1"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AATTGTACGG

10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C2 - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTCCCCCTGTA CGG

13

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer C1 - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCTTCAGCT

10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer PEPCivs#9 - forward"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTACAAAAAC CAGCAACTC

19

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer PEPCivs#9 reverse"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCACAAAG TGGAGTAGT

19

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer P7(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGGTGAAGGG CCCCGGCTTC ACCGG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer P8(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATCATCGATG AGCTCCTACA CCTGATCGAT GTGGTA

36

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer for fourth quarter - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCAGGAGCT CATCGATGAT

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer for third quarter - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCCCCCTGT A

11

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK23A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGCTGCGG ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK25A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGCTGACCC TGACCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK26A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACCTGATGG ACATCCTGAA

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "sequence in pCIB3073 prior to deletion"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TATAAGGATC CCGGGGGCAA GATCTGAGAT ATG

33

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE134A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTGACCGAC TACCACATCG ATCAAGTATC CAATTAGTT GAGT

44

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE135A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACTCAACTAA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG

44

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer KE136A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT

37

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer KE137A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTGATTATG CATCAGCCTA T

21

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer KE138A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTG

38

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK05A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CAAAGGTACC CAATAGCGTA ACG

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer MK35A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AACGAGGTGT ACATCGACCG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "forward primer for pCIB4434"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACCGATAT CACCATCCAA GGAGGGATG ACGTATTCAA AG

42

202964  
(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "reverse primer for  
pCIB4434"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGCGCATCGA TTGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G

51

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATTACGTTAC GCTATTGGGT ACCTTTGATG

30

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA

60

TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGA

98

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CAAGTGCAGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGGAACCCGG ACCTAGACTG

60

CAGCTGCAGG GACGGGGAAA AATGTGCCCA TCATTCCC

98

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #4"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGTTTCTCT TCGAGAAATT CTAGATTCC

30

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer used to map  
transcriptional start site for TrpA gene"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCGTTCGTTC CTCCTTCGTC GAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..26  
(D) OTHER INFORMATION: /note= "N-terminal peptide from  
pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr	Thr	Pro	Leu	Thr	Phe	Gln	Val	Gly	Lys	Ser	Lys	Pro	Gly	His
1					5			10				15		
Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile					
		20					25							

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "internal peptide of pollen  
specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys	Pro	Gly	His	Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile	Ser	Asp
1					5				10			15			

Val Val Ile Lys  
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /note= "internal peptide from  
pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Gly Gly Thr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..12  
(D) OTHER INFORMATION: /note= "internal peptide from  
pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu His Gly Gly Asp Asp Phe Ser Phe Thr Leu Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Glu Gly Pro Thr Gly Thr Trp Thr Leu Asp Thr Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide #51"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AARTCRTCAB CACCRGYTC

20

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide #58"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCCCA CYTGRAA

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide PE51"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TGGCCCATGG CTGCGCGGG GAACGAGTGC GGC

33

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #42"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGCGGTGAC CTGCAGGCAT GCGATCTGCA CCTCCCGCCG

40

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer #43"

- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGGCAAGG AGCTCGGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #SK50"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCTTCAAAA TCTAGAAACC T

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer #SK49"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TAATGTCGAC GAACGGCGAG AGATGGA

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE99A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCGGTTACC GCCGATCAC A TG

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE97A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCGGTACCGC GTCGACGCGG ATCCCGCGGC GGGAAAGCTAA G

41

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE100A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCGTCGACC GCAACA

16

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE98A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC

39

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE104A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATGTCGTG ACCGCAACAC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE103A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGTACCGC GGATCCTGTC CGACACCGGA CGGCT

35

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE127"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCGGATCCGG CTGCGGCGGG GAACGA

26

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE150A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATTCGCATGC ATGTTTCATT ATC

23

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer KE151A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCTGGTACCA CGGATCCGTC GCTTCTGTGC AACAAACC

37